

SEQUENCE LISTING

<110> Dickey, Lynn
Gasdaska, John
Cox, Kevin

<120> Expression of Biologically Active
Polypeptides in Duckweed

<130> 40989/267934

<150> US 09/915,873

<151> 2001-07-26

<150> US 60/293,330

<151> 2001-05-23

<150> US 60/221,705

<151> 2000-07-31

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 554

<212> DNA

<213> Zea mays

<400> 1
gatcaagtgc aaaggtccgc cttgtttctc ctctgtctct tgatctgact aatcttggtt 60
tatgattcgt tgagtaattt tggggaaagc ttcgtccaca gttttttttt cgatgaacag 120
tgccgcagtg gcgctgatct tgtatgctat cctgcaatcg tggatgaactt atgtctttta 180
tattccttcac taccatgaaa agactagtaa tctttctcga tgtaacatcg tccagcactg 240
ctattaccgt gtggtccatc cgacagtctg gctgaacaca tcatacgata ttgagcaaag 300
atctatcttc cctgttcttt aatgaaagac gtcattttca tcagtatgat ctaagaatgt 360
tgcaacttgc aaggaggcgt ttctttcttt gaatttaact aactcgttga gtggccctgt 420
ttctcggacg taaggccttt gctgctccac acatgtccat tcgaatttta ccgtgttttag 480
caagggcgaa aagtttgcac cttgatgatt tagcttgact atgacgattgc tttcctggac 540
ccgtgcagct gcgg 554

<210> 2

<211> 498

<212> DNA

<213> Artificial Sequence

<220>

<223> Duckweed codon optimized nucleotide sequence
encoding human alpha-2B interferon

<221> CDS

<222> (1)...(498)

<400> 2
tgc gac ctc ccc cag acc cac agc ctc ggg tcc cgc cgc acc ctc atg 48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1 5 10 15
ctg ctg gcg cag atg cgc cgc atc tcg ctc ttc agc tgc ctg aag gac 96
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30
cgc cac gac ttc ggc ttc ccg cag gag gag ttc ggc aac cag ttc cag 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45
aag gcc gag acg atc ccc gtg ctc cac gag atg atc cag cag atc ttc 192
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60
aac ctg ttc agc acc aag gac agc tcg gcc gcc tgg gac gag acc ctg 240
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80
ctc gac aag ttc tac acc gag ctg tac cag cag ctc aac gac ctg gag 288
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95
gcg tgc gtg atc cag ggg gtt ggg gtt acg gag acg ccg ctg atg aag 336
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
100 105 110
gag gac agc atc ctc gcc gtg cgc aag tac ttc cag cgc atc acg ctc 384
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125
tac ctc aag gag aag aag tac agc ccg tgc gcc tgg gag gtc gtt cgc 432
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140
gcc gag atc atg cgc tcc ttc agc ctg agc acc aac ctc cag gag agc 480
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145 150 155 160
ctc cgc tcc aag gag taa 498
Leu Arg Ser Lys Glu *
165

<210> 3

<211> 96

<212> DNA

<213> Oryza sativa

<400> 3

accatgcagg tcctgaacac gatgggtcaac aagcacttcc tctccctgtc cgtcctcatc 60
gtcctcctcg ggctgagcag caacctcacc gccggc 96

<210> 4
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
 1 5 10 15
 Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
 20 25 30
 Gly Ser Arg Arg Thr Leu Met Leu Ala Gln Met Arg Arg Ile Ser
 35 40 45
 Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
 50 55 60
 Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
 65 70 75 80
 Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
 85 90 95
 Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
 100 105 110
 Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 115 120 125
 Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
 130 135 140
 Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
 145 150 155 160
 Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
 165 170 175
 Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
 180 185

<210> 5
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 5
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1 5 10 15
 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20 25 30
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35 40 45
 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50 55 60
 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65 70 75 80
 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85 90 95
 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
 100 105 110
 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
 115 120 125
 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
 3

130 135 140
 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
 145 150 155 160
 Leu Arg Ser Lys Glu
 165

<210> 6
 <211> 31
 <212> PRT
 <213> *Oryza sativa*

<400> 6
 Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
 1 5 10 15
 Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly
 20 25 30

<210> 7
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Modified rice alpha-amylase signal peptide

<400> 7
 Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
 1 5 10 15
 Val Leu Ile Val Leu Thr Val Leu Ser Ser Asn Leu Thr Ala Gly
 20 25 30

<210> 8
 <211> 21
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 8
 Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
 1 5 10 15
 Leu Ser Ser Ala Glu
 20

<210> 9
 <211> 498
 <212> DNA
 <213> *Homo sapiens*

<400> 9
 tgtgatctgc ctcaaaccga cagcctgggt agcaggagga ccttgatgct cctggcacag 60
 atgaggagaa tctctctttt ctcttgcttg aaggacagac atgacttttg atttccccag 120
 gaggagtttg gcaaccagtt ccaaaaggct gaaaccatcc ctgtcctcca tgagatgata 180
 cagcagatct tcaatctctt cagcacaag gactcatctg ctgcttggga tgagaccctc 240

ctagacaaat tctacactga actctaccag cagctgaatg acctggaagc ctgtgtgata 300
cagggggtgg gggtagacaga gactcccctg atgaaggagg actccattct ggctgtgagg 360
aaatacttcc aaagaatcac tctctatctg aaagagaaga aatacagccc ttgtgcctgg 420
gaggttgtca gagcagaaaat catgagatct ttttctttgt caacaaactt gcaagaaagt 480
ttaagaagta aggaatga 498

<210> 10
<211> 569
<212> DNA
<213> Homo sapiens

<400> 10
atggccttga cctttgcttt actggtggcc ctctggtgc tcagctgcaa gtcaagctgc 60
tctgtgggct gtgatctgcc tcaaaccac agcctgggta gcaggaggac cttgatgctc 120
ctggcacaga tgaggagaat ctctcttttc tcctgcttga aggacagaca tgactttgga 180
tttccccagg aggagtttgg caaccagttc caaaaggctg aaaccatccc tgcctccat 240
gagatgatcc agcagatctt caatctcttc agcacaaagg actcatctgc tgcttgggat 300
gagacctcc tagacaaatt ctacactgaa ctctaccagc agctgaatga cctggaagcc 360
tgtgtgatac aggggggtgg ggtgacagag actcccctga tgaaggagga ctccattctg 420
gctgtgagga aatacttcca aagaatcact ctctatctga aagagaagaa atacagccct 480
tgtgcctggg aggttgtcag agcagaaatc atgagatctt tttctttgtc aacaaacttg 540
caagaaagtt taagaagtaa ggaatgaaa 569

<210> 11
<211> 62
<212> DNA
<213> Arabidopsis thaliana

<400> 11
atgaagacta atctttttct ctttctcatc ttttcacttc tcctatcatt atcctcggcc 60
ga 62

<210> 12
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(78)
<223> Duckweed codon optimized sequence encoding hGH
signal peptide

<223> Duckweed codon optimized hGH signal peptide

<400> 12
atg gcg acc ggg tcc cgc acc tcc ctc ctc ctg gcc ttc ggc ctg ctc 48
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15
tgc ctg ccc tgg ctc cag gag ggc tcc gcg 78
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
20 25

<210> 13

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<400> 13
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Ala Phe Gly Leu Leu
      1          5          10          15
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
      20          25

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<220>
<221> CDS
<222> (1)...(573)
<223> Duckweed codon optimized sequence encoding mature
      hGH
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[illegible]

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 Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
 130 135 140
 aag ttc gac acc aac agc cac aac gac gac gcc ctc ctc aag aac tac 480
 Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
 145 150 155 160
 ggg ctg ctc tac tgc ttc cgg aag gac atg gac aag gtc gag acc ttc 528
 Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
 165 170 175
 ctc cgc atc gtg cag tgc cgc tcc gtg gag ggc tcc tgc ggc ttc 573
 Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

<210> 15
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 15
 Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
 1 5 10 15
 Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
 20 25 30
 Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
 35 40 45
 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
 50 55 60
 Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
 65 70 75 80
 Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
 85 90 95
 Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
 100 105 110
 Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
 115 120 125
 Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
 130 135 140
 Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
 145 150 155 160
 Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
 165 170 175
 Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

<210> 16
 <211> 63
 <212> DNA
 <213> Lemna gibba

<400> 16
gaaactcccg aggtgagcaa ggatccggag tcgagcgcga agaagagaaa gagggaaagc 60
gcg 63